

Title: ' US-09-988-201-5

RESULT 1

ACCGKAB

LOCUS ACCGKAB 2180 bp DNA linear BCT 21-APR-1994

DEFINITION A.carrageenovora genes cgkA and cgkB, partial.

ACCESSION X71620

VERSION X71620.1 GI:437973

KEYWORDS kappa-carrageenase.

SOURCE Pseudoalteromonas carrageenovora

ORGANISM Pseudoalteromonas carrageenovora

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

Alteromonadaceae; Pseudoalteromonas.

REFERENCE

1

AUTHORS Barbeyron,T., Henrissat,B. and Kloareg,B.

TITLE The gene encoding the kappa-carrageenase of Alteromonas

carrageenovora is related to beta-1,3-1,4-glucanases

JOURNAL Gene 139 (1), 105-109 (1994)

MEDLINE 94156170

PUBMED 8112578

REFERENCE 2 (bases 1 to 2180)

AUTHORS Barbeyron,T.

TITLE Direct Submission

JOURNAL Submitted (15-APR-1993) T. Barbeyron, CNRS, Place George Teissier,

29680 Roscoff, FRANCE

FEATURES

Location/Qualifiers

source

1. .2180

/organism="Pseudoalteromonas carrageenovora"

/mol\_type="genomic DNA"

/strain="ATCC 43555"

/db\_xref="taxon:227"

/clone="pKA1,pKA2,pKA3,pKA4"

gene

557. .1934

/gene="cgkA"

-35\_signal

557. .562

/gene="cgkA"

-10\_signal

581. .586

/gene="cgkA"

RBS

726. .729

/gene="cgkA"

CDS

741. .1934

/gene="cgkA"

/codon\_start=1

/transl\_table=11

/product="kappa-carraghenase"

/protein\_id="CAA50624.1"

/db\_xref="GI:437974"

/db\_xref="SWISS-PROT:P43478"

/translation="MKPISIVAFPIPAISMLLLSAVSQAASMQPPIAKPGETWILQAK

RSDEFNVKDATKWNFQTENYGVWSWKNNATVSNGLKLTKKRESHQRTFWDGCNQQQ

VANYPLYTSGVAKSRATGNYGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVQ

YSEIDVVELTQKSAVRESHDHLHNI VVKNGKPTWMRPGSFPTNHNGYHLPFDPRNDF

HTYGVNVTKDKITWYVDGEIVGEKDNLYWHRQMNLTLSQLRAPHTQWKCNQFYPSAN

KSAEGFPTSMEVDYVRTWVKVGNNSAPGEGQSCPNFTFVAVNSVQLSAAKQTLRKGQS

TTLESTVLPNCATNKKVIYSSSNKNVATVNSAGVVAKNKGTTATITVKTKNKGKIDKL

TIQVN"

sig\_peptide

741. .815

/gene="cgkA"

gene

2000. .2180

/gene="cgkB"

RBS

2000. .2004

/gene="cgkB"

CDS

2009. .>2180

/gene="cgkB"

/codon\_start=1

/transl\_table=11

/protein\_id="CAA50625.1"

/db\_xref="GI:437975"

/db\_xref="SWISS-PROT:P43479"

/translation="MKKVNLSKWIISISLLIICDYVYLIRTNVNEQANAETAHMHY

KINNTKHSKGKLD"

BASE COUNT        787 a     397 c     420 g     576 t  
ORIGIN

Query Match                100.0%;   Score 2180;   DB 1;   Length 2180;  
Best Local Similarity    100.0%;   Pred. No. 0;  
Matches 2180;   Conservative    0;   Mismatches    0;   Indels       0;   Gaps        0;

```
Qy      1  GATCATATCATTCCTTTGCAAATTAAAAATTCTCAAGATAGTCAAATAATTAGTTTTTTT 60
      |||
Db      1  GATCATATCATTCCTTTGCAAATTAAAAATTCTCAAGATAGTCAAATAATTAGTTTTTTT 60

Qy     61  AAAGCTGACAAAGGGAGTGTGAGCAGGCAAGTACACCCACCTTGGCCTGTGCCTTGTA 120
      |||
Db     61  AAAGCTGACAAAGGGAGTGTGAGCAGGCAAGTACACCCACCTTGGCCTGTGCCTTGTA 120

Qy    121  AGTAAACTGCAAGAGCAAGATAGTAGTGAGTCTAAAGAGAGTAAGGCAGAGCAAGTTAA 180
      |||
Db    121  AGTAAACTGCAAGAGCAAGATAGTAGTGAGTCTAAAGAGAGTAAGGCAGAGCAAGTTAA 180

Qy    181  ATTAACAACTGCGTTGTACAGAACGCAATGCTGTACATAGAAAACAATTATTTCAACGAT 240
      |||
Db    181  ATTAACAACTGCGTTGTACAGAACGCAATGCTGTACATAGAAAACAATTATTTCAACGAT 240

Qy    241  ATAAATATAGACACGGTTGCTTTTTCTGTTGGCGTAAGTCGCTCTTATCTCGTTAAACA 300
      |||
Db    241  ATAAATATAGACACGGTTGCTTTTTCTGTTGGCGTAAGTCGCTCTTATCTCGTTAAACA 300

Qy    301  TTTAAGTTAGCAACGAATAAAACGATTAATAATAGAATCATAGAAGTAAGAATAGAGCAG 360
      |||
Db    301  TTTAAGTTAGCAACGAATAAAACGATTAATAATAGAATCATAGAAGTAAGAATAGAGCAG 360

Qy    361  GCTAAAAAAGTATTACTAAAAAATCTGTTACAGAAACAGCTTATGAAGTTGGTTTTAAT 420
      |||
Db    361  GCTAAAAAAGTATTACTAAAAAATCTGTTACAGAAACAGCTTATGAAGTTGGTTTTAAT 420

Qy    421  AACTCAAACACTTTCGCGACAGTTTTTAAAAAAGAACAACACTACACGCCCAAGCAATTT 480
      |||
Db    421  AACTCAAACACTTTCGCGACAGTTTTTAAAAAAGAACAACACTACACGCCCAAGCAATTT 480

Qy    481  AAACGTACTTTTTCCAGCTAAACACTACAATAACGATTAAGGCCATTTTTAGAGA 540
      |||
Db    481  AAACGTACTTTTTCCAGCTAAACACTACAATAACGATTAAGGCCATTTTTAGAGA 540

Qy    541  ACAGTAAACCATTTTTTGAGGTTTGGTGTTGTATATAAATATTAAATATCCCCACTCGC 600
      |||
Db    541  ACAGTAAACCATTTTTTGAGGTTTGGTGTTGTATATAAATATTAAATATCCCCACTCGC 600

Qy    601  TCAGCTTTTTTTGTGCGAGTTGTGAGAATTAGCTTAACAGGTAAGGTTTACGTATCTGTA 660
      |||
Db    601  TCAGCTTTTTTTGTGCGAGTTGTGAGAATTAGCTTAACAGGTAAGGTTTACGTATCTGTA 660

Qy    661  TATCTAAACTCTTCGAATATAACACTGTATCTGTTGCTGAGCTGTGGCTCAGTTCACACT 720
      |||
Db    661  TATCTAAACTCTTCGAATATAACACTGTATCTGTTGCTGAGCTGTGGCTCAGTTCACACT 720

Qy    721  AACAAAGGATGGATAAATAAATGAAACCTATAAGTATTGTGGCATTCCCTATACCAGCTA 780
      |||
Db    721  AACAAAGGATGGATAAATAAATGAAACCTATAAGTATTGTGGCATTCCCTATACCAGCTA 780

Qy    781  TAAGTATGCTTCTTTTAAGTGCAGTATCACAAGCAGCATCTATGCAACCTCCCATCGCAA 840
      |||
Db    781  TAAGTATGCTTCTTTTAAGTGCAGTATCACAAGCAGCATCTATGCAACCTCCCATCGCAA 840

Qy    841  AACCTGGTGAAACATGGATTTTACAAGCCAAACGCTCTGACGAATTTAACGTAAAAGATG 900
      |||
Db    841  AACCTGGTGAAACATGGATTTTACAAGCCAAACGCTCTGACGAATTTAACGTAAAAGATG 900

Qy    901  CGACAAAGTGGAACCTTCAAACAGAAAACATATGGGGTATGGTCTTGAAAAATGAAAATG 960
      |||
Db    901  CGACAAAGTGGAACCTTCAAACAGAAAACATATGGGGTATGGTCTTGAAAAATGAAAATG 960
```

Qy	961	CGACAGTATCTAATGGCAAACATAAATAAACCCTAAGCGAGAATCTCATCAACGTACAT	1020
Db	961	CGACAGTATCTAATGGCAAACATAAATAAACCCTAAGCGAGAATCTCATCAACGTACAT	1020
Qy	1021	TCTGGGATGGCTGTAATCAGCAGCAAGTTGCAAATTACCCACTTTATTATACATCGGGTG	1080
Db	1021	TCTGGGATGGCTGTAATCAGCAGCAAGTTGCAAATTACCCACTTTATTATACATCGGGTG	1080
Qy	1081	TCGCTAAATCCAGAGCTACAGGTAATTATGGCTATTACGAAGCTCGAATCAAAGGAGCGA	1140
Db	1081	TCGCTAAATCCAGAGCTACAGGTAATTATGGCTATTACGAAGCTCGAATCAAAGGAGCGA	1140
Qy	1141	GTACATTTCTGGCGTATCGCCTGCTTTTTGGATGTATAGCACCATTGACCGTTCATTAA	1200
Db	1141	GTACATTTCTGGCGTATCGCCTGCTTTTTGGATGTATAGCACCATTGACCGTTCATTAA	1200
Qy	1201	CGAAAGAAGGGGATGTCCAATATAGCGAAATAGACGTAGTGGAACCTACTCAAAAAAGTG	1260
Db	1201	CGAAAGAAGGGGATGTCCAATATAGCGAAATAGACGTAGTGGAACCTACTCAAAAAAGTG	1260
Qy	1261	CAGTGAGAGAGTCTGATCATGACTTACACAATATTGTAGTAAAAATGGAAAACCAACAT	1320
Db	1261	CAGTGAGAGAGTCTGATCATGACTTACACAATATTGTAGTAAAAATGGAAAACCAACAT	1320
Qy	1321	GGATGCGTCCAGGGTCTTTTCCGCAGACAAATCATAACGGATACCATCTACCTTTTCGATC	1380
Db	1321	GGATGCGTCCAGGGTCTTTTCCGCAGACAAATCATAACGGATACCATCTACCTTTTCGATC	1380
Qy	1381	CTCGAAATGACTTTCACACCTATGGTGTCAATGTAAGTAAAGACAAGATCACTTGGTACG	1440
Db	1381	CTCGAAATGACTTTCACACCTATGGTGTCAATGTAAGTAAAGACAAGATCACTTGGTACG	1440
Qy	1441	TAGATGGTGAAATTGTGGGCGAAAAGGATAACTTATACTGGCATCGTCAAATGAATCTCA	1500
Db	1441	TAGATGGTGAAATTGTGGGCGAAAAGGATAACTTATACTGGCATCGTCAAATGAATCTCA	1500
Qy	1501	CATTATCACAAGGCTTACGCGCGCCGCATACACAATGGAAATGTAATCAATTTTACCCAT	1560
Db	1501	CATTATCACAAGGCTTACGCGCGCCGCATACACAATGGAAATGTAATCAATTTTACCCAT	1560
Qy	1561	CAGCGAATAAATCAGCAGAAGGCTTCCCAACATCAATGGAAGTTGATTATGTAAGAACGT	1620
Db	1561	CAGCGAATAAATCAGCAGAAGGCTTCCCAACATCAATGGAAGTTGATTATGTAAGAACGT	1620
Qy	1621	GGGTAAAGGTGGGCAATAACAACCTCTGCTCCAGGCGAGGGGCAGTCATGTCCTAACACGT	1680
Db	1621	GGGTAAAGGTGGGCAATAACAACCTCTGCTCCAGGCGAGGGGCAGTCATGTCCTAACACGT	1680
Qy	1681	TTGTAGCTGTCAATAGTGTTCAACTAAGCGCAGCAAAACAAACACTTCGAAAGGGCCAAT	1740
Db	1681	TTGTAGCTGTCAATAGTGTTCAACTAAGCGCAGCAAAACAAACACTTCGAAAGGGCCAAT	1740
Qy	1741	CTACAACGCTAGAAAGCACAGTTCTTCCAAACTGTGCAACCAACAAGAAAGTCATTTATT	1800
Db	1741	CTACAACGCTAGAAAGCACAGTTCTTCCAAACTGTGCAACCAACAAGAAAGTCATTTATT	1800
Qy	1801	CATCAAGCAATAAAAATGTGGCAACTGTGAACAGTGCTGGCGTTGTAAAAGCTAAAAATA	1860
Db	1801	CATCAAGCAATAAAAATGTGGCAACTGTGAACAGTGCTGGCGTTGTAAAAGCTAAAAATA	1860
Qy	1861	AAGGCACTGCGACGATTACGGTTAAACATAAAACAAAGGGAAAATAGATAAATTAACCA	1920
Db	1861	AAGGCACTGCGACGATTACGGTTAAACATAAAACAAAGGGAAAATAGATAAATTAACCA	1920
Qy	1921	TTGCGGTGAATTAAGCTAACTCAAACCTAGCCTCGAAGGATTGAGGCACTTTATTTATAGG	1980
Db	1921	TTGCGGTGAATTAAGCTAACTCAAACCTAGCCTCGAAGGATTGAGGCACTTTATTTATAGG	1980
Qy	1981	TCTCAGGCTTCGACTTTTTGGAGGGGGTATGAAAAAGGTAAATTTATCCAGCAAGTGGAT	2040
Db	1981	TCTCAGGCTTCGACTTTTTGGAGGGGGTATGAAAAAGGTAAATTTATCCAGCAAGTGGAT	2040

Qy	2041	AATTAGCATTAGTTTACTAATCATTGTGATTATGTTTATTTAATACGAACAAACGTTAA	2100
Db	2041	AATTAGCATTAGTTTACTAATCATTGTGATTATGTTTATTTAATACGAACAAACGTTAA	2100
Qy	2101	CGAGCAAGCTAACGCAGAAGCTACTGCACATATGCATTACAAAATAAATAATACGAAACA	2160
Db	2101	CGAGCAAGCTAACGCAGAAGCTACTGCACATATGCATTACAAAATAAATAATACGAAACA	2160
Qy	2161	CTCAAAAGGAAAGCTTGATC	2180
Db	2161	CTCAAAAGGAAAGCTTGATC	2180

Title: US-09-988-201-6

RESULT 1

I39507

kappa-carraghenase - *Alteromonas carrageenovora*

C;Species: *Alteromonas carrageenovora*

C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 08-Oct-1999

C;Accession: I39507; S40202

R;Barbeyron, T.; Henrissat, B.; Kloareg, B.

Gene 139, 105-109, 1994

A;Title: The gene encoding the kappa-carrageenase of *Alteromonas carrageenovora* is related to beta-1,3-1,4-glucanases.

A;Reference number: I39507; MUID:94156170; PMID:8112578

A;Accession: I39507

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-397 <RES>

A;Cross-references: EMBL:X71620; NID:g437973; PIDN:CAA50624.1; PID:g437974

C;Genetics:

A;Gene: cgkA

Query Match 64.9%; Score 2116; DB 2; Length 397;  
Best Local Similarity 100.0%; Pred. No. 7e-136;  
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	167	MKPISIVAFPIPAISMLLLSAVSQAASMQPPIAKPGETWILQAKRSDEFNVKDATKWNFQ	226
Db	1	MKPISIVAFPIPAISMLLLSAVSQAASMQPPIAKPGETWILQAKRSDEFNVKDATKWNFQ	60
Qy	227	TENYGVWSWKNNENATVSNGLKLTTKRESHQRTFWDGCNQQQVANYPLYTSGVAKSRAT	286
Db	61	TENYGVWSWKNNENATVSNGLKLTTKRESHQRTFWDGCNQQQVANYPLYTSGVAKSRAT	120
Qy	287	GNYGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVQYSEIDVVELTQKSAVRES DH	346
Db	121	GNYGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVQYSEIDVVELTQKSAVRES DH	180
Qy	347	DLHNIVVKNGKPTWMRPGSFPQTNHNGYHLPFDP RND FHTYGVNVTKDKITWYVDGEIVG	406
Db	181	DLHNIVVKNGKPTWMRPGSFPQTNHNGYHLPFDP RND FHTYGVNVTKDKITWYVDGEIVG	240
Qy	407	EKDNL YWHRQMNL T L S QGLRAPHTQWKCNQFYPSANKSAEGFPTSMEVDYVRTWVKVGNN	466
Db	241	EKDNL YWHRQMNL T L S QGLRAPHTQWKCNQFYPSANKSAEGFPTSMEVDYVRTWVKVGNN	300
Qy	467	NSAPGEGQSCPNTFVAVNSVQLSAAKQTLRKQSTTLESTVLPNCATNKKVIYSSSNKNV	526
Db	301	NSAPGEGQSCPNTFVAVNSVQLSAAKQTLRKQSTTLESTVLPNCATNKKVIYSSSNKNV	360
Qy	527	ATVNSAGVVKAKNKG TATITVKTKNKGKIDKLTIAVN	563
Db	361	ATVNSAGVVKAKNKG TATITVKTKNKGKIDKLTIAVN	397